

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	311	100.0	311	4	US-09-634-955B-5 Sequence 5, Appli
2	311	100.0	311	4	US-09-816-760-5 Sequence 5, Appli
3	311	100.0	311	4	US-09-838-561-5 Sequence 5, Appli
4	52	16.7	311	4	US-09-838-561-15 Sequence 15, Appli
5	9	2.9	682	4	US-09-107-532A-4499 Sequence 4499, Ap
6	9	2.9	1170	4	US-09-462-136-6 Sequence 6, Appli
7	8	2.6	113	3	US-08-905-223-439 Sequence 439, App
8	8	2.6	261	4	US-09-328-352-7731 Sequence 7731, Ap
9	8	2.6	263	4	US-09-270-767-46093 Sequence 46093, A
10	8	2.6	299	4	US-09-902-540-14916 Sequence 14916, A
11	8	2.6	310	4	US-09-907-794A-153 Sequence 153, App
12	8	2.6	310	4	US-09-905-125A-153 Sequence 153, App
13	8	2.6	310	4	US-09-902-775A-153 Sequence 153, App
14	8	2.6	310	4	US-09-906-700-153 Sequence 153, App
15	8	2.6	310	4	US-09-903-603A-153 Sequence 153, App
16	8	2.6	310	4	US-09-904-920A-153 Sequence 153, App
17	8	2.6	310	4	US-09-909-064-153 Sequence 153, App

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1607	100.0	311	4	US-09-634-955B-5	Sequence 5, Appli
2	1607	100.0	311	4	US-09-816-760-5	Sequence 5, Appli
3	1607	100.0	311	4	US-09-838-561-5	Sequence 5, Appli
4	1467	91.3	311	4	US-09-838-561-15	Sequence 15, Appl
5	651.5	40.5	310	4	US-09-907-794A-153	Sequence 153, App
6	651.5	40.5	310	4	US-09-905-125A-153	Sequence 153, App
7	651.5	40.5	310	4	US-09-902-775A-153	Sequence 153, App
8	651.5	40.5	310	4	US-09-906-700-153	Sequence 153, App
9	651.5	40.5	310	4	US-09-903-603A-153	Sequence 153, App
10	651.5	40.5	310	4	US-09-904-920A-153	Sequence 153, App
11	651.5	40.5	310	4	US-09-909-064-153	Sequence 153, App
12	651.5	40.5	310	4	US-09-905-381A-153	Sequence 153, App
13	651.5	40.5	310	4	US-09-906-618-153	Sequence 153, App

Database :       UniProt\_03:\*

          1: uniprot\_sprot:\*

          2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	52	16.7	223	2	Q8CHS7	Q8chs7 mus musculu
2	9	2.9	281	1	CG11_RAT	P97586 rattus norv
3	9	2.9	1170	2	Q12200	Q12200 saccharomyc
4	8	2.6	83	1	YORC_TTV1	P19287 thermoprote
5	8	2.6	134	2	Q89T92	Q89t92 bradyrhizob
6	8	2.6	137	2	Q6ZTJ1	Q6ztj1 homo sapien
7	8	2.6	150	2	Q747K4	Q747k4 geobacter s
8	8	2.6	216	2	Q72RN4	Q72rn4 leptospira
9	8	2.6	216	2	Q8F428	Q8f428 leptospira
10	8	2.6	226	2	Q8MT30	Q8mt30 drosophila
11	8	2.6	233	2	Q9CHT7	Q9cht7 lactococcus
12	8	2.6	235	2	Q6XHS1	Q6xhs1 drosophila
13	8	2.6	237	2	Q6IDG8	Q6idg8 drosophila
14	8	2.6	244	2	Q8D3B0	Q8d3b0 wiggleswort

Database : PIR\_79:\*

1: pirl:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		%	Match	Length	
1	9	2.9	1170	2	S52525 probable membrane
2	8	2.6	233	2	G86703 oxidoreductase ygc
3	8	2.6	260	2	E70881 probable fabG5 pro
4	8	2.6	261	2	G82082 conserved hypothet
5	8	2.6	262	2	T34378 hypothetical prote
6	8	2.6	293	2	T19954 hypothetical prote
7	8	2.6	325	2	T17307 hypothetical prote
8	8	2.6	341	2	D70761 probable fatty-acy
9	8	2.6	371	2	A44122 alpha-helical coil
10	8	2.6	938	2	T34105 hypothetical prote
11	8	2.6	964	2	AG3433 diguanylate cyclas
12	7	2.3	135	2	G89751 protein C33E10.10
13	7	2.3	141	2	C97338 hydroxymyristoyl-(
14	7	2.3	146	2	G97030 probable membrane
15	7	2.3	148	2	F86899 hypothetical prote
16	7	2.3	151	2	D75347 hypothetical prote
17	7	2.3	157	2	C71477 probable ribityllu
18	7	2.3	167	2	D82561 probable signal pe
19	7	2.3	184	2	B72601 hypothetical prote
20	7	2.3	198	2	B82080 flavodoxin [simila
21	7	2.3	200	2	T42066 glutamate-ammonia

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		%	Match	Length	DB	
1	640.5	39.9	325	2	T17307	hypothetical prote
2	311.5	19.4	537	2	T34380	hypothetical prote
3	307	19.1	262	2	T34378	hypothetical prote
4	299.5	18.6	278	2	E83152	probable short-cha
5	274	17.1	277	2	AG1983	hypothetical prote
6	265.5	16.5	263	2	AI1692	oxidoreductase hom
7	265.5	16.5	266	2	H97309	short-chain alcoho
8	255.5	15.9	263	2	AH1321	oxidoreductase hom
9	253	15.7	259	2	A69965	ketoacyl reductase
10	249	15.5	259	2	B83838	oxidoreductase BH1
11	245	15.2	293	2	AD2176	oxidoreductase all
12	242	15.1	270	2	E86788	oxidoreductase yne
13	241.5	15.0	328	2	F75374	probable ketoacyl
14	241	15.0	247	2	F90254	hypothetical prote
15	241	15.0	253	2	A95223	hypothetical prote
16	238.5	14.8	287	2	C55210	hetN protein - Ana
17	235.5	14.7	287	2	AF2475	ketoacyl reductase
18	234.5	14.6	307	2	E70082	glucose 1-dehydrog
19	234	14.6	261	1	A28788	actinorhodin polyk
20	233	14.5	332	2	S37652	follicular lymphom

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 12, 2005, 13:06:08 ; Search time 174 Seconds  
(without alignments)  
915.268 Million cell updates/sec

Title: US-10-664-506-5  
Perfect score: 1607  
Sequence: 1 MGVMAMILMLPLLLLGISGLL.....FFFAVVACGVKEKLNVPEEG 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1017	63.3	223	2	Q8CHS7	Q8chs7 .mus musculu
2	651.5	40.5	310	2	Q6UX59	Q6ux59 homo sapien
3	651.5	40.5	325	2	Q9BTF9	Q9btf9 homo sapien
4	650.5	40.5	325	2	Q6IAN0	Q6ian0 homo sapien
5	640.5	39.9	325	2	Q9UFM6	Q9ufm6 homo sapien
6	625.5	38.9	323	2	Q99J47	Q99j47 m similar t
7	557	34.7	291	2	Q9Y3A1	Q9y3a1 homo sapien
8	466	29.0	326	2	Q9Y140	Q9y140 drosophila
9	458	28.5	317	2	Q7Q732	Q7q732 anopheles g
10	331	20.6	311	2	Q65ZI3	Q65zi3 caenorhabdi
11	322	20.0	264	2	Q81M93	Q81m93 bacillus an
12	321	20.0	264	2	Q635E8	Q635e8 bacillus ce
13	320	19.9	264	2	Q731G1	Q731g1 bacillus ce
14	311.5	19.4	537	2	Q22787	Q22787 caenorhabdi
15	309	19.2	264	2	Q6HE26	Q6he26 bacillus th

16	302.5	18.8	268	2	Q6F8F2	Q6f8f2 acinetobact
17	299.5	18.6	278	2	Q9HX59	Q9hx59 pseudomonas
18	295.5	18.4	339	1	DHS7_HUMAN	Q9y394 homo sapien
19	295.5	18.4	375	2	Q659E8	Q659e8 homo sapien
20	290.5	18.1	267	2	Q8EJM5	Q8ejm5 shewanella
21	288.5	18.0	324	2	Q6I7R1	Q6i7r1 rattus norv
22	286.5	17.8	260	2	O15744	O15744 dictyosteli
23	282	17.5	338	1	DHS7_MOUSE	Q9cxr1 mus musculu
24	277	17.2	273	2	Q6W1F0	Q6w1f0 rhizobium s
25	276	17.2	336	2	Q6GP08	Q6gp08 xenopus lae
26	274	17.1	277	2	Q8YX01	Q8yx01 anabaena sp
27	271	16.9	268	2	Q6CNU5	Q6cnu5 kluyveromyc
28	265.5	16.5	263	2	Q92A39	Q92a39 listeria in
29	265.5	16.5	266	2	Q97DY5	Q97dy5 clostridium
30	263	16.4	298	2	Q87XV8	Q87xv8 pseudomonas
31	262.5	16.3	260	2	Q65HP3	Q65hp3 bacillus li
32	260.5	16.2	263	2	Q71Y45	Q71y45 listeria mo
33	258	16.1	312	2	Q9N126	Q9n126 bos taurus
34	258	16.1	316	2	Q8T197	Q8t197 dictyosteli
35	256	15.9	280	2	Q65F58	Q65f58 bacillus li
36	255.5	15.9	248	2	Q9RH22	Q9rh22 zymomonas m
37	255.5	15.9	263	2	Q8Y5S9	Q8y5s9 listeria mo
38	254	15.8	303	2	Q6F7B8	Q6f7b8 acinetobact
39	253	15.7	259	1	YQJQ_BACSU	P54554 bacillus su
40	253	15.7	295	2	Q8RR58	Q8rr58 acinetobact
41	252	15.7	295	2	P94129	P94129 acinetobact
42	250.5	15.6	271	2	Q7UPD8	Q7upd8 rhodopirell
43	249.5	15.5	311	2	Q9NYR8	Q9nyr8 homo sapien
44	249	15.5	259	2	Q9KCR3	Q9kcr3 bacillus ha
45	247	15.4	276	2	Q9ALU7	Q9alu7 enterobacte

## ALIGNMENTS

### RESULT 1

Q8CHS7

ID Q8CHS7 PRELIMINARY; PRT; 223 AA.  
 AC Q8CHS7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Similar to CGI-86-protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RA Strausberg R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -!!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.  
 DR EMBL; BC03'9565; AAH39565.1; -.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR002347; Adh\_short\_C2.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00081; GDHRDH.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 223 AA; 25088 MW; 368381EADF415B90 CRC64;

Query Match 63.3%; Score 1017; DB 2; Length 223;  
 Best Local Similarity 90.7%; Pred. No. 4.2e-76;  
 Matches 194; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy	98 LDLSDISCVPDVAKEVLDCYGCVDILINNASVKVKGPAHKISLELDKKIMDANYFGPITL	157
	:	
Db	10 VDLSDISCVQDVAKEVLDCYGCVDILINNASVKVKGPAHKISLELDKKIMDANYFGPITL	69
	:              :	
Qy	158 TKALLPNMISRRTGQIVLVNNIQGKFGIPFRRTYAASKHAALGFFDCLRAEVEEYDVVIS	217
	:              :	
Db	70 TKVLLPNMISRRTGQIVLVNNIQAKFGIPFRRTAYAASKHAVMGFFDCLRAEVEEYDVVIS	129
Qy	218 TVSPTFIRSYHVYPEQGNWEASIWKFFFRKLTYGVHPVEAEEVMRTVRRKKQEVFMNP	277
	:	
Db	130 TVSPTYIIRSYRASPEQRNWETSICKFFCRKLAYGVHPVEAEEVMRTVRRKKQEVFMNP	189
Qy	278 IPKAAYVVRTFFFPEFFFVAVVACGVKEKLNVPEEG	311
	:     :	
Db	190 VPKAAYFIRTFFFPEFFFVAVVACGVKEKLNVPEEG	223

RESULT 2

Q6UX59

ID Q6UX59 PRELIMINARY; PRT; 310 AA.

AC Q6UX59;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE DFIT212.  
 GN ORFNames=UNQ212;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270 (2003).  
 CC -!!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.  
 DR EMBL; AY358498; AAQ88862.1; -.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR002347; Adh\_short\_C2.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00081; GDHRDH.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 310 AA; 33524 MW; 5BE703478EE20BD7 CRC64;  
  
 Query Match 40.5%; Score 651.5; DB 2; Length 310;  
 Best Local Similarity 43.5%; Pred. No. 1.2e-45;  
 Matches 138; Conservative 59; Mismatches 89; Indels 31; Gaps 6;  
  
 Qy 3 VMAMMLPLLL--LGISGLLFIFYQEVSRLWSKSAVQNKKVVITDAISGLGKECARVFHTG 60  
 : : : |||| ||: || : | | : ::| ||||| | ||||||| : ||:  
 Db 4 ITSTAILPPLLFGCLGVFGLFRLQQWVR---GKAYLRNAVVIITGATSGLGKEAKVFYAA 60  
  
 Qy 61 GARLVLCGKNWERLENLYDAL-ISVADPSKTFTPVLVLLDLSDISCVPDVAKEVLDGYGC 119  
 ||:|||||: ||| | | | : | | ||| ||: : | | :| | :| |:  
 Db 61 GAKLVLCGRNNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAIVAAAAEILQCFGY 120  
  
 Qy 120 VDILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTAKLLPNMISRRTGQIVLVNNI 179  
 ||||:||| : : | : ::::|::|: | |||||: |||||||:||| | | | | :|:  
 Db 121 VDILVNNAGISYRGTIMDTTVDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSI 180  
  
 Qy 180 QGKFGIPFRRTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIR---SYHVYPEQGNW 236

Db            |||    ||||: |||||||    |||||::|:|:: :|| :| :    | :  
181 QGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGS- 239

Qy            237 EASIWKFFFRLTYGV-----HPVEVAEEVMRTVRRKKQEVFMANPIPKAAVYVRT 287  
              |||            |||||::|:| :||::| :| :| |||:||

Db            240 -----RYGVMDTTAQGRSPVEVAQDVLAAGVKKKDVLADLLPSLAVYLRT 287

Qy            288 FFPEFFFAVVACGVKEK 304  
              | ||::| : :::

Db            288 LAPGLFFSLMASRARKE 304

## RESULT 3

## Q9BTF9

ID    Q9BTF9        PRELIMINARY;        PRT;        325 AA.  
AC    Q9BTF9;  
DT    01-JUN-2001 (TrEMBLrel. 17, Created)  
DT    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT    25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE    DKFZP5660084 protein.  
GN    Name=DKFZp5660084;  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    TISSUE=Lung;  
RX    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA    Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA    Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA    Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA    Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA    Jones S.J., Marra M.A.;  
RT    "Generation and initial analysis of more than 15,000 full-length human  
RT    and mouse cDNA sequences.";  
RL    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN    [2]  
RP    SEQUENCE FROM N.A.  
RC    TISSUE=Lung;  
RA    Strausberg R.;  
RL    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
RN    [3]  
RP    SEQUENCE FROM N.A.  
RC    TISSUE=Lung;

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	311	100.0	311	4	AAB47593	Aab47593 Human DHD
2	311	100.0	311	6	ABP58046	Abp58046 Human deh
3	311	100.0	311	8	ADG40199	Adg40199 Human deh
4	255	82.0	311	3	AAB08911	Aab08911 Human sec
5	255	82.0	345	3	AAB08948	Aab08948 Human sec
6	156	50.2	246	8	ADM33425	Adm33425 Human PRO
7	107	34.4	118	4	AAM24151	Aam24151 Human EST
8	70	22.5	81	8	ABO54789	Abo54789 Human gen
9	52	16.7	311	6	ABP58047	Abp58047 Mouse deh
10	52	16.7	311	8	ADG40201	Adg40201 Mouse deh
11	29	9.3	29	3	AAB08949	Aab08949 Human sec
12	9	2.9	31	6	ADA98202	Ada98202 Human sec
13	9	2.9	31	6	ADA44050	Ada44050 Human sec
14	9	2.9	31	7	ADC20368	Adc20368 Human sec
15	9	2.9	31	7	ADF10701	Adf10701 Human sec
16	9	2.9	32	4	AAB60717	Aab60717 Human sec
17	9	2.9	281	2	AAW38423	Aaw38423 Rat cell
18	9	2.9	281	7	ADE62861	Ade62861 Rat Prote

RESULT 4

AAB08911

ID AAB08911 standard; protein; 311 AA.

XX

AC AAB08911;

XX

DT 30-AUG-2000 (first entry)

XX

DE Human secreted protein sequence encoded by gene 21 SEQ ID NO:68.

XX

KW Human; secreted protein; cytostatic; anti-proliferative; vulnerary;  
KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;  
KW hyperproliferative disorder; infectious disease; tissue regeneration;  
KW screening; food additive; preservative; wound healing;  
KW hyper-vascular disease; chromosome 11.

XX

OS Homo sapiens.

XX

PN WO200017222-A1.

XX

PD 30-MAR-2000.

XX

PF 22-SEP-1999; 99WO-US022012.

XX

PR 23-SEP-1998; 98US-0101546P.

PR 02-OCT-1998; 98US-0102895P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;  
PI Komatsoulis G, Endress GA, Soppet DR;

XX

DR WPI; 2000-283538/24.

DR N-PSDB; AAA39072.

XX

PT Human secreted proteins and coding sequences useful in diagnostic and  
PT therapeutic methods for disorders such as immune system or proliferative  
PT disorders, related to the proteins.

XX

PS Claim 11; Page 366-367; 416pp; English.

XX

CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the  
CC human secreted proteins given in AAB08891 to AAB08984.. The human secreted  
CC proteins can have activities based on the tissues and cells they are  
CC expressed in. Examples of the activities are: cytostatic; anti-  
CC proliferative; immunosuppressive; antibacterial; and vulnerary. The  
CC secreted proteins and their related polynucleotide sequences are useful  
CC for diagnostic and therapeutic methods useful for diagnosing and treating  
CC disorders related to the secreted proteins. The proteins, and  
CC polynucleotide sequences may be useful for treating disorders of the  
CC immune system, hyperproliferative disorders, infectious disease,  
CC regeneration of tissues, for chemotaxis and for screening molecules that  
CC bind to the proteins. The proteins or polynucleotide sequences may be  
CC used as food additives or preservatives, to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, co-factors or other nutritional components. Agonists or  
CC antagonists of the proteins may be used to prevent scar tissue growth

CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051  
CC and AAB08890 are sequences used in the exemplification of the present  
CC invention

xx

SQ Sequence 311 AA;

Query Match 82.0%; Score 255; DB 3; Length 311;  
Best Local Similarity 100.0%; Pred. No. 2e-231;  
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGVMAMILMLPLLLLGISGLLFIFYQEVSRLWSKSAVQNKKVVITDAISGLGKECARVFHTG 60

Db 1 MGVMAMLMLP<sub>1</sub>LLLGI SGLLFI YQEVSRLWSKS<sub>1</sub>VQNKVVVITDAI SGLGKECARVFHTG 60

Qy 61 GARLVLCGKNWERLENLYDALISVADPSKTFPKLVLLDSLSCVPDVAKEVLD CYGCV 120

Db 61 GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDI SCVPDVAKEVLDYGCV 120

Qy 121 DILINNASVKVKGPAHKISLELDKKIMDANYFGPI TLTKALLPNMISRRTGQIVLVNNIQ 180

Db 121 DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ 180

Qy 181 GKFGI PFRRTTYAASKHAALGFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI 240

Db 181 GKFGI PFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRS YHVYPEQGNWEASI 240

.Qy 241 WKFFFRLTYGVHPV 255

..... | | | | | | | | | | | | | | | | | |

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	311	100.0	311	9	US-09-838-561-5	Sequence 5, Appli
2	311	100.0	311	9	US-09-816-760-5	Sequence 5, Appli
3	311	100.0	311	14	US-10-172-585-5	Sequence 5, Appli
4	311	100.0	311	15	US-10-144-433-2	Sequence 2, Appli
5	311	100.0	311	15	US-10-664-506-5	Sequence 5, Appli
6	311	100.0	311	15	US-10-144-433-2	Sequence 2, Appli
7	255	82.0	311	9	US-09-820-893-68	Sequence 68, Appli
8	255	82.0	311	15	US-10-607-565-68	Sequence 68, Appli
9	255	82.0	345	9	US-09-820-893-106	Sequence 106, App
10	255	82.0	345	15	US-10-607-565-106	Sequence 106, App

RESULT 1  
AI091419/c  
LOCUS AI091419 631 bp mRNA linear EST 30-OCT-1998  
DEFINITION ow62e03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
IMAGE:1651420 3' similar to WP:T25G12.7 CE07544 DEHYDROGENASE  
;contains TAR1.t3 MER22 repetitive element ;, mRNA sequence.  
ACCESSION AI091419  
VERSION AI091419.1 GI:3430478  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 631)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1044 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 453.  
FEATURES Location/Qualifiers  
source 1..631  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1651420"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from five normalized  
libraries were mixed, and ss circles were made in vitro.  
Following HAP purification, this DNA was used as tracer in  
a subtractive hybridization reaction. The driver was  
PCR-amplified cDNAs from pools of 5,000 clones made from  
the same 5 libraries. The pools consisted of the following  
libraries and cloneIDs: Soares NbHSF pool 1:  
309384-310919, 323208-325895 Soares Nb2HP pool 1:  
145032-147335, 147720-148103, 148872-149255, 15002 -  
150407, 151176-152327 Soares Nb2HF8-9W pool 1:  
758280-760583, 772104-774407 Soares NbHPA pool 1:  
304776-306311, 320136-322823, 326280-326663 Soares NbHOT  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
-----  
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## ORIGIN

Query Match 45.0%; Score 621; DB 1; Length 631;  
Best Local Similarity 100.0%; Pred. No. 5.9e-294;  
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 698 TCATCAACAAATGCCAGTGTGAAGGTGAAGGGCCTGCCCCATAAGATTTCTCTGGAGCTCG 757

Db 621 TCATCAACAATGCCAGTGTGAAGGTGAAGGGCCTGCCATAAGATTCTCTGGAGCTCG 562  
Qy 758 ACAAAAAGATCATGGATGCCAATTACTTGGCCCCATCACATTGACGAAAGCCCTGCTTC 817  
|||  
Db 561 ACAAAAAGATCATGGATGCCAATTACTTGGCCCCATCACATTGACGAAAGCCCTGCTTC 502  
Qy 818 CCAACATGATCTCCGGAGAACAGGCCAATCGTGTAGTGAATAATATCCAAGGGAAGT 877  
|||  
Db 501 CCAACATGATCTCCGGAGAACAGGCCAATCGTGTAGTGAATAATATCCAAGGGAAGT 442  
Qy 878 TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGCTTCTTG 937  
|||  
Db 441 TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGCTTCTTG 382  
Qy 938 ACTGCCTCCGAGCGAAGTGGAGGAATACGATGTTGTATCAGCACCGTGAGCCGACTT 997  
|||  
Db 381 ACTGCCTCCGAGCGAAGTGGAGGAATACGATGTTGTATCAGCACCGTGAGCCGACTT 322  
Qy 998 TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTGGAAAT 1057  
|||  
Db 321 TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTGGAAAT 262  
Qy 1058 TCTTTTCAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGC 1117  
|||  
Db 261 TCTTTTCAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGC 202  
Qy 1118 GCACCGTGCAGGAGGAAGAACAGAGGTGTTATGCCAACCCATCCCCAAGGCCCG 1177  
|||  
Db 201 GCACCGTGCAGGAGGAAGAACAGAGGTGTTATGCCAACCCATCCCCAAGGCCCG 142  
Qy 1178 TGTACGTCCGCACCTTCTTCCGGAGTTCTTTCGCGTGGTGGCCTGTGGGGTGAAGG 1237  
|||  
Db 141 TGTACGTCCGCACCTTCTTCCGGAGTTCTTTCGCGTGGTGGCCTGTGGGGTGAAGG 82  
Qy 1238 AGAAGCTCAATGTCCGGAGGAGGGTAACGCAGGAGGCCAAATGGGCCACCCCTTGG 1297  
|||  
Db 81 AGAAGCTCAATGTCCGGAGGAGGGTAACGCAGGAGGCCAAATGGGCCACCCCTTGG 22  
Qy 1298 AATAAAGGTTTCTGGCAA 1318  
|||  
Db 21 AATAAAGGTTTCTGGCAA 1

## ORIGIN

```

Query Match          40.0%;  Score 551;  DB 1;  Length 632;
Best Local Similarity 99.8%;  Pred. No. 1.7e-259;
Matches 601;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy 705 CAATGCCAGTGTGAAGGTGAAGGGCCTGCCATAAGATTCTCTGGAGCTCGACAAAAAA 764

Db 615 CAATGCCAGTGTGAAGGTGAAGGGCCTGCCATAAGATTCTCTGGAGCTGACAGAAA 556  
Qy 765 GATCATGGATGCCAATTACTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCAAACAT 824  
|||  
Db 555 GATCATGGATGCCAATTACTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCAAACAT 496  
Qy 825 GATCTCCCGAGAACAGGCCAATCGTGTAGTAATAATATCCAAGGAAAGTTGGAAT 884  
|||  
Db 495 GATCTCCCGAGAACAGGCCAATCGTGTAGTAATAATATCCAAGGAAAGTTGGAAT 436  
Qy 885 CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGACGCCCTGGGCTTCTTGACTGCCT 944  
|||  
Db 435 CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGACGCCCTGGGCTTCTTGACTGCCT 376  
Qy 945 CCGAGCCGAAGTGGAGGAATACGATGTTGTATCAGCACCGTGAGCCGACTTCATCCG 1004  
|||  
Db 375 CCGAGCCGAAGTGGAGGAATACGATGTTGTATCAGCACCGTGAGCCGACTTCATCCG 316  
Qy 1005 GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTGGAAATTCTTTT 1064  
|||  
Db 315 GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTGGAAATTCTTTT 256  
Qy 1065 CAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT 1124  
|||  
Db 255 CAGGAAGCTGACCTACGGCGTGCACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT 196  
Qy 1125 GCGGAGGAAGAACAGAGGTGTTATGGCAACCCATCCCCAAGGCCGCCGTGTACGT 1184  
|||  
Db 195 GCGGAGGAAGAACAGAGGTGTTATGGCAACCCATCCCCAAGGCCGCCGTGTACGT 136  
Qy 1185 CCGCACCTTCTTCCGGAGTTCTTCGCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT 1244  
|||  
Db 135 CCGCACCTTCTTCCGGAGTTCTTCGCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT 76  
Qy 1245 CAATGTCCCGAGGAGGGTAACGCAGGAGGCCAATGGGCCACCCCTGGAAATAAG 1304  
|||  
Db 75 CAATGTCCCGAGGAGGGTAACGCAGGAGGCCAATGGGCCACCCCTGGAAATAAG 16  
Qy 1305 GT 1306  
|||  
Db 15 GT 14

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1379	100.0	1379	4	AAH43561	Aah43561 Human DHD
2	1379	100.0	1379	10	ABV76050	Abv76050 Human deh
3	1379	100.0	1379	12	ADG40198	Adg40198 cDNA enco
4	1004	72.8	1114	8	ABX71069	Abx71069 Novel hum
5	955	69.3	1157	3	AAA39072	Aaa39072 Human sec
6	936	67.9	936	4	AAH43565	Aah43565 Human DHD
7	677	49.1	797	12	ADM33424	Adm33424 Human PRO
8	327	23.7	780	4	AAH98810	Aah98810 Human EST
9	208	15.1	247	12	ACH82344	Ach82344 Human gen
10	208	15.1	514	12	ACH68644	Ach68644 Human gen
c 11	159	11.5	599	12	ACH69248	Ach69248 Human gen

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
<hr/>					
1	1379	100.0	1379	6 AR278046	AR278046 Sequence
2	1379	100.0	1379	6 AR392052	AR392052 Sequence
3	1379	100.0	1379	6 AR403912	AR403912 Sequence
4	1379	100.0	1379	6 AX320639	AX320639 Sequence
5	1004	72.8	1114	6 AR542048	AR542048 Sequence
6	955	69.3	1157	6 BD233739	BD233739 31 human
7	933	67.7	933	6 AR278047	AR278047 Sequence
8	933	67.7	933	6 AR392053	AR392053 Sequence
9	933	67.7	933	6 AR403913	AR403913 Sequence
10	933	67.7	933	6 AX320641	AX320641 Sequence
11	932	67.6	932	6 CQ731016	CQ731016 Sequence
12	451	32.7	188646	9 AC027045	AC027045 Homo sapi

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_htc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
c 1	621	45.0	631	1	AI091419	AI091419 ow62e03.x
c 2	551	40.0	632	1	AI741629	AI741629 wg28f07.x
c 3	495	35.9	562	1	AI458236	AI458236 tj53e07.x
c 4	485	35.2	632	1	AI741640	AI741640 wg28g07.x
5	478	34.7	483	9	AY421548	AY421548 Homo sapi
c 6	473	34.3	473	1	AI376903	AI376903 tc27f05.x
c 7	469	34.0	469	1	AI141463	AI141463 qa67d12.x
c 8	414	30.0	558	1	AI222126	AI222126 qh02g04.x
c 9	261	18.9	505	1	AA953672	AA953672 oo02e08.s
10	257	18.6	309	7	F26544	F26544 HSPD14061 H
c 11	256	18.6	307	1	AI470361	AI470361 tj42f03.x
c 12	254	18.4	477	1	AI168267	AI168267 oo10c10.x
13	248	18.0	267	9	AY421549	AY421549 Pan trogl
14	247	17.9	274	7	F35823	F35823 HSPD32901 H
c 15	243	17.6	396	1	AA928254	AA928254 on79a08.s
c 16	222	16.1	480	1	AI022337	AI022337 ow95a11.x